

Appl. No. : 10/063,710
Filed : May 8, 2002

AMENDMENTS TO THE CLAIMS

1-3. (Canceled).

4. (Currently Amended) An isolated nucleic acid having at least 95% nucleic acid sequence identity to a sequence of interest selected from the group comprising:

(a) the nucleic acid sequence of SEQ ID NO:75;

(b) the full-length coding sequence of the nucleic acid sequence of SEQ ID NO:75; and ~~or~~

(c) the full-length coding sequence of the cDNA deposited under ATCC accession number 203247;

wherein said nucleic acid is more highly expressed in esophageal tumor tissue compared to normal esophageal tissue; and

wherein said nucleic acid sequence identity between the isolated nucleic acid and the sequence of interest is determined without introducing a gap into either of the nucleotide sequences being compared, so as to increase the number of aligned nucleotides.

5. (Currently Amended) The isolated nucleic acid of Claim 4 having at least 99% nucleic acid sequence identity to a sequence of interest selected from the group comprising:

(a) the nucleic acid sequence of SEQ ID NO:75;

(b) the full-length coding sequence of the nucleic acid sequence of SEQ ID NO:75; and ~~or~~

(c) the full-length coding sequence of the cDNA deposited under ATCC accession number 203247;

wherein said nucleic acid is more highly expressed in esophageal tumor tissue compared to normal esophageal tissue; and

wherein said nucleic acid sequence identity between the isolated nucleic acid and the sequence of interest is determined without introducing a gap into either of the nucleotide sequences being compared, so as to increase the number of aligned nucleotides.

6. (Previously Presented) An isolated nucleic acid comprising:

(a) the nucleic acid sequence of SEQ ID NO:75;

(b) the full-length coding sequence of the nucleic acid sequence of SEQ ID NO:75; or

(c) the full-length coding sequence of the cDNA deposited under ATCC accession number 203247.

7-10. (Canceled).

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11. (Previously Presented) The isolated nucleic acid of Claim 6 comprising the nucleic acid sequence of SEQ ID NO:75.

12. (Previously Presented) The isolated nucleic acid of Claim 6 comprising the full-length coding sequence of the nucleic acid sequence of SEQ ID NO:75.

13. (Original) The isolated nucleic acid of Claim 6 comprising the full-length coding sequence of the cDNA deposited under ATCC accession number 203247

14-16. (Canceled).

17. (Previously Presented) A vector comprising the nucleic acid of Claim 4.

18. (Original) The vector of Claim 17, wherein said nucleic acid is operably linked to control sequences recognized by a host cell transformed with the vector.

19. (Previously Presented) An isolated host cell comprising the vector of Claim 17.

20. (Original) The host cell of Claim 19, wherein said cell is a CHO cell, an E. coli or a yeast cell.

21-25. (Canceled).

26. (Currently Amended) An isolated nucleic acid having at least 95% nucleic acid sequence identity to a sequence of interest selected from the group comprising:

(a) the nucleic acid sequence of SEQ ID NO:75;

(b) the full-length coding sequence of the nucleic acid sequence of SEQ ID NO:75; and ~~or~~

(c) the full-length coding sequence of the cDNA deposited under ATCC accession number 203247;

wherein said nucleic acid hybridizes to the complement of a nucleic acid of SEQ ID NO: 75 under conditions of 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C; and

wherein said nucleic acid sequence identity between the isolated nucleic acid and the sequence of interest is determined without introducing a gap into either of the nucleotide sequences being compared, so as to increase the number of aligned nucleotides.

27. (Currently Amended) The isolated nucleic acid of Claim 26 having at least 99% nucleic acid sequence identity to a sequence of interest selected from the group comprising:

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(a) the nucleic acid sequence of SEQ ID NO:75;
(b) the full-length coding sequence of the nucleic acid sequence of SEQ ID NO:75; and or
(c) the full-length coding sequence of the cDNA deposited under ATCC accession number 203247;

wherein said nucleic acid hybridizes to the complement of a nucleic acid of SEQ ID NO: 75 under conditions of 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C; and

wherein said nucleic acid sequence identity between the isolated nucleic acid and the sequence of interest is determined without introducing a gap into either of the nucleotide sequences being compared, so as to increase the number of aligned nucleotides.

28. (Previously Presented) A vector comprising the nucleic acid of Claim 26.

29. (Previously Presented) The vector of Claim 28, wherein said nucleic acid is operably linked to control sequences recognized by a host cell transformed with the vector.

30. (Previously Presented) An isolated host cell comprising the vector of Claim 28.

31. (Previously Presented) The host cell of Claim 30, wherein said cell is a CHO cell, an E. coli or a yeast cell.

32. (New) The isolated nucleic acid of Claim 4 having at least 96% nucleic acid sequence identity to a sequence of interest selected from the group comprising:

(a) the nucleic acid sequence of SEQ ID NO:75;
(b) the full-length coding sequence of the nucleic acid sequence of SEQ ID NO:75; and
(c) the full-length coding sequence of the cDNA deposited under ATCC accession number 203247;

wherein said nucleic acid is more highly expressed in esophageal tumor tissue compared to normal esophageal tissue; and

wherein said nucleic acid sequence identity between the isolated nucleic acid and the sequence of interest is determined without introducing a gap into either of the nucleotide sequences being compared, so as to increase the number of aligned nucleotides.